

## **FIGURE 1**

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCAGGGCTGCTAGGCCTC  
TGTGCCCGGGCTTGAATTGGTGCAGGATGCCAGCTCCGGATGACCCGCCGGACCCGCT  
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGC  
GTTTGGCCCAGGACGGGGCCATGTGGTCGTCAAGCAGCCGAAGCAGCAGAATGTGGACCAG  
GCGGTGGCCACGCTGCAGGGGAGGGCTGAGCGTGACGGCACCGTGTGCCATGTGGGAA  
GGCGGAGGACCGGGAGCGGCTGGCACGGCTGTGAAGCTTATGGAGGTATCGATATCC  
TAGTCTCCAATGCTGCTGTCAACCCTTCTTGAAAGCATAATGGATGTCAGTGAGGAGGTG  
TGGGACAAGACTCTGGACATTAATGTGAAGGCCAGCCCTGATGACAAAGGCAGTGGTGC  
AGAAATGGAGAACGAGGAGGCAGCTCAGTGGTATCGTGTCTTCCATAGCAGCCTCAGTC  
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTGCTGGCCTGACCAAGACC  
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAACCTGCCTAGCACCTGGACTTATCAA  
GAATAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC  
TGCAGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTCTGTGCTCT  
GAAGATGCCAGCTACATCACTGGGAAACAGTGGTGGTGGAGGAACCCGTCCGCCT  
CTGAGGACCGGGAGACAGCCCACAGGCCAGAGTTGGCTCTAGCTCCTGGTGTCTGC  
ATTCAACCACTGGCTTCCCACCTCTGCTCACCTACTGTTCACCTCATCAAATCAGTTCT  
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTACTCGGGATTCTGCT  
GTTGTTGTGGCTTGGTAAAGGCCTCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT  
GAGTCTACCTGGCAAAGACCAAGATATTTTCTGGCCACTGGTGAATCTGAGGGGTGA  
TGGGAGAGAAGGAACCTGGAGTGGAGGAGCAGAGTTGCAAATTAAACAGCTTGCAAATGAGG  
TGCAAATAAAATGCAGATGATTGCGCGGCTTGAaaaaaaaaaaaaaa

## **FIGURE 2**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672
><subunit 1 of 1, 278 aa, 1 stop
><MW: 29537, pI: 8.97, NX(S/T): 1
MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVVS
SRKQQNVDQAVATLQGEGLSVTGTVCVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation site.**

amino acids 183-186

**N-myristoylation sites.**

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 276-278

### FIGURE 3

GC GCCCTGAGCTCGCCTCCGGGCCGATAGCGGCATCGAGAGCGCCTCCGTGAGGACCAGGGCG  
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCTCGAGAACCAAGGTGGC  
GCGGCTGGAGGAGGAGAACCGAGACTTCTGGCTCGCCTGGAGGACGCC**ATGG**AGCAGTACAAACTGC  
AGAGCGACCGGCTGCGTGAGCAGCAGGAGGAGATGGTGAAC TGCGGCTGCGTTAGAGCTGGTGC  
CCAGGCTGGGGGGCCTCGGGCTCCTGAATGGCCTGCCTCCGGTCCTTGTGCCTCGACCTCATAC  
AGCCCCCTGGGGGTGCCACGCCATGTCTGGCATGGTGCCTGCCTGCCTGGAGATG  
AAGTTGGCTCTGAGCAGAGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT  
GAGGTGAACAGGCTGGGAAGTGGCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGCC  
CAGGGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGAGGCC  
GGAGTCTGCCAGAGAGGAAGGGCCAGAGCTTGCCTTGAGGAGTTGGATGCCAGCCATTCCAGGGTCC  
AGAGCAGTTGGTGGGAGCAAGGCCAGTTCAAGGAGCTGGCTATCAACATCCGATGAAGGAGGAGCTTA  
TGCGAGCTGGTCCGCACAGGAAGGCAGCTCAGGCCCTGAACCGCAGCACAGCCAGCGTATCCG  
GAGCTGGAGCAGGAGGAGCAGCAGGTGCGGCCAGCTGAGTGAAGGCCAGAGGCAGCTGCC  
CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCAGGAGTTCCGCAGGAGGGCG  
CGGCCAGGCCAGGTGCAGGTGCTGAAGGAGAAGAACGAGCTACGGAGCGCTGGTGTACTGTC  
GCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGAACGTGCAGCTCATGCCAGCAGCAGGGACA  
GCTGCAGAGGCCGCTCGCAGGAGACGGAGCAGAACGGCGCTGGAGGCAGAAATGAGCAAGCG  
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGAACAGCAGAACAGATCTGAAGATTAAAGACGGAA  
GAGATCGCGGCCCTCCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAGCCTGG  
GCAGAACAGATTGAGGAGCAGAACAGTGGCTGGACCAGGAGATGGAGAACGGTGC  
CGCTGGAGGAGCTGGGAGGAGCTCCACAAGCGGGAGGCCATCTGGCCAAGAACGG  
CAGGAGAACAGGGCTGGAGAGAACGCCCTCAACGAGGACATCG  
AGTGTCCAGGCCGCTGGAGCACCTGGAGAACGGAGCTGCTCGAGAACGG  
GCGCCAGGCCAGCAGCAGATCCGGGGAGATCGACAGCCTGCCAGGAGAACGG  
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGAGCTGCTGT  
GCTGTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAAC  
CATGCCAGGGTCTCGGCCCTCAGCTCGTGTCCCAGTGCAGATGAAC  
AAGCTCAGCTACCTCTCATCCTCAGAGAACGCCCTCTGCAAGTATTT  
GCTCCAGAGGAGCAGCACAGCAGAACATTGCCCTCGGA  
AGAGGCTGGTACTGGCTGGAGGCTGGAGCAGGCCAGCTGACC  
CTGCAGCAGAACGGAGCAGGAGCAGAACATGCAGCTGCTCCTGCAG  
AGGGTTAGCAGACAGCAGGAGGAGTATGAGGCCGGATTCAAG  
ACATGTGGATAAACCAAGAACAGAACAGAACGG  
GGGGAGAACAGGAGGCCCTGTGCTGGAGGGCAGAACGG  
ACCCGAGCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCG  
TGGTCACGCTCCGTACCCCTGACCTGGAAACGCTCGAGC  
GAGGAACGTAGGGCAGCGGGAGGCAGCTGGAGCC  
CCTGCCCTGGAACATTGGCCTTGTCCAAGGCCGG  
TTGATGTCCGGAAAACCCCTG**TAA**AGCCCTGGGG  
GCTGAAAGGGCAGCTGCCCTGTTGTGAAGGG  
CCCTCATCTGTACCCCTCACTGGGATCAACAA  
AACAAAATAATGCAAATTCCCACCA  
TCTTGCTCGAATCTCAGGACAATTCTGG  
GCCAAGAACATCACGAAAGGGTGG  
GAAACTGGAGACTT  
GAGGATCTT  
AAAAAACCA  
TTA  
AAAAAAAT  
CTTGAAGGGAC

10032169 122704

## **FIGURE 4**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465  
<subunit 1 of 1, 830 aa, 1 stop  
<MW: 95029, pI: 8.26, NX(S/T): 2  
MEQYKLQSDRLREQQEEMVELRLRLELVRPGWGLRLNLPPGSFVPRPHTAPLGGAHAV  
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL  
HLRRNRISNCQRAGARPGSLPERKGPELCLEELDAAIPGSRAVGGSKARVQARQVPPATAS  
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE  
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVSLSAQSEKRLQE  
LERNVQLMRQQQGQLQRRLREETEQKRRLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA  
AFQRKRRSGSNGSVVSLEQQQKIEEQQKWLQEMEKVLQQRALEELGEELHKREAILAKKE  
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAQSQQQIRGEIDS  
LRQEKDSSLKQRLEIDGKLQRGSLLSPEEERTLFQLDEAI EALDAAI EYKNEAITCRQRVLR  
ASASLLSQCEMNLMALKSYLSSSETRALLCKYFDKVVTLREEHQHQQIAFSELEMQLEEQQR  
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLQQSRDHLGEGLADSRRQYEARIQALEK  
ELGRYMWINQELKQKLGGVNAVGHSGRKSLCSEGRQAPGNEDELHLAPELLWLSPTEG  
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG  
PLSKPRRELRRASPGMIDVRKNPL

**Important features:**

**Leucine zipper pattern.**

amino acids 557-579, 794-815

**N-glycosylation sites.**

amino acids 133-136, 383-386

**Kinesin related protein Kif-4 Coiled-coil domain:**

amino acids 231-672

## **FIGURE 5**

ATTCTCCTAGAGCATTTGGAAGCATGAGGCCACGATGCTGCATCTGGCTTGCTGCT  
GGATAACAGTCTTCCTCCAGTGTCAAAGGAAC<sup>T</sup>ACAGACGCTCCTGGCTCAGGA  
CTGTGGCTGTGCCAGCGACACCCAGGTGTGGAAACAAGATCTACAACCCTTCAGAGCAGTG  
CTGTTATGATGATGCCATCTTATCCTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT  
TCTGGCCCTGCTTGAGCTCTGCTGTCCCAGTCTTTGGCCCCAGCAGAAGTTCTTGTG  
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCGGAGCTGTAC  
CAGGAACAGGAGGCACGTCTGTACCCAAAACCCAGGCTCCACTGGCAGACGGCAGAC  
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAAC<sup>T</sup>TCGGAGAGAAGCA  
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTGGAGAGGAGGCCAGCTGGGATGGC  
CAGACTTCAGGGGAAGAATGCCTCCTGCTTCATCCCCTTCCAGCTCCCTCCGCTGAG  
AGCCACTTCATCGGCAATAAAATCCCCACATTACCATCT

## **FIGURE 6**

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
><subunit 1 of 1, 125 aa, 1 stop
><MW: 14198, pI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLLQCSKGTTDAPVGSGLWLQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRLGMKSQCHLSPISRSCTRNRRHVLYP
```

**Important features:**

**Signal sequence**

amino acids 1-21

**N-myristoylation sites.**

amino acids 33-39, 70-76

## **FIGURE 7**

CCACCGCGTCCGCCACCGTCCGGTGCACACTCGCGCCGCCGCTCCGGCTTCCTCT  
TTTCCCTCCGACGCCACGGCTGCCAGACATTCCGGCTGCCGGTCTGGAGAGCTCCCCG  
AACCCCTCCGGAGAGGGAGCGAGGCCGGAGGATGAGCGACTGAGGGCGACGCCGACTGACCGAGTT  
GGGCCGCGACTACCGCAGCTGACAGCGCATGAGCGACTCCCCAGAGACGCCCTAGCCCG  
GTGTGCGGCCAGGCCAGGGAGCGCGCAGGTGGGCTGGCTTAGTGGTCCGCCAACGCCGG  
TCGCCGGCCGCCAGGATGGCGCTGGCAACCCGGCCGCCGCGCTGCTACCCCTG  
CGCCCGCTGCGAGCCCGCGTCCGGCCCGCCCTGCGCTCATGGACGCCGGCTCCCGCC  
GCCGGCGCGCCCGGGCTGTGAATGCGACTCGCCCCTGGCCCGCTCCCCGCCGCC  
GCCCGCCGGACGTGGTAGGG**G**CCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA  
GTTCCCTCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCGCTGGAG  
AAGCTGGCCAGGCACCAGAGCAGCCGGCAGGAGAAGCGTGAGCACGCCACTCGGACGG  
CCCGGGCGGGTAACGAGCTGGCGCCGGCAGGGACGAGGGCGAGCGGGCGACT  
GGAAGAGCAAGAGCGGCCGTGGCTGCCGGCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC  
TGGGTCTCCCAGGGCGGGGCCAAGGCCGGGATCTGCAGGTCCGGCCCCGCCGGACAC  
CCCGCAGGCCAGCCCTGGCCGCAGCCGCCAGGACGCGATTGGCCCGAACTCGGCCCA  
CGCCCGAGCCACCGAGGAGTACGTGTACCGGACTACCGTGGCAAGGGCTGCGTGGACGAG  
AGCGGCTTCGTGTACCGATCGGGAGAAGTTCGCGCCGGCCCTCGCCCTGCCGTGCCT  
GTGCACCGAGGGAGGGCCGCTGTGCAGCCGAGTGCAGGCCGAGGCTGCACCCGCCGTGCA  
TCCACGTCGACACGAGCCAGTGCTGCCCGCAGTGCAGGAGAGGAAGACTACTGCGAGTTC  
CGGGCAAGACCTATCAGACTTGGAGGAGTTCGTGGTCTCCATGCGAGAGGTGTCGCTG  
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTCAAGCGTGTCCCCAGACGGAGTGTGGACC  
CTGTGTACGAGCCTGATCAGTGTCTGCCATCTGCAAAATGGTCAAAGTGCCTTGAGAA  
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC  
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC  
**AAATGTAGACGCTTCCCAGAACACAAACTCTGACTTTCTAGAACATTTACTGATGTGAA**  
CATTCTAGATGACTCTGGAACTATCAGTCAAAGAAGACTTTGATGAGGAATAATGGAAAA  
TTGTTGGTACTTTCTTCTTGATAACAGTTACTACAACAGAAGGAATGGATATATTTC  
AAAACATCAACAAGAACATTGGCATAAAATCCCTCTAAATAATGTGCTATTTCACAG  
TAAGTACACAAAGTACACTATTATATCAAATGTATTCTATAATCCCTCCATTAGAGAG  
CTTATATAAGTGTCTATAGATGCAGATTAAATGCTGTGTCAACCGTAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSTAMAVGALSSSLVTCLMVALCSPSIPLEKLAQAPEQPGQEKRHATRDGPGRVNEL  
GRPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQAEALA  
AAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDESGFVYAI GEKFAPGPSACPCLCTEEGPL  
CAQPECPR LHPRCIHV DTSQCCPQCKERKNYCEFRGKYQTLEEFVVSP CERCRCEANGEVL  
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEEGTWR  
IERQAMCTRHECRQM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187

## **FIGURE 9**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGTTCATCCTCCCAC  
TGCCAGGAGTGCAGGCCTGCTCTGCCAGTTGGGACAGTTCAAGCATGTGTGGAAGGTGTCC  
GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTGGGTGCCAGGA  
CACGTTGATGCTCATTGAGAGCGGACCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
AGGCCAAGGACCAGGAGCCCCCGCTCACTGAGCACGGATGGGCCCTCTCCCTGATC  
TCCTACACCTCGTGTGCCGCCAGGAGGACTCTGCAACAAACCTCGTTAACTCCCTCCGCT  
TTGGGCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG  
AAGGCTGTCTGGAGGGACAACAGAAGAGATCTGCCCAAGGGACCACACACTGTTATGAT  
GGCCTCCTCAGGCTCAGGGAGGAGGCATCTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
CCAGCCAGGTTGCAACCTGCTCAATGGACACAGGAAATTGGGCCGTGGTATGACTGAGA  
ACTGCAATAGGAAAGATTTCTGACCTGTCATCGGGGACCACCAATTGACACACAGGAAAC  
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCAGGT  
GTGTCAAGGAGACGCTGCTGTCATAGATGTAGGACTCACATCAACCCCTGGTGGGACAAAAG  
GCTGCAGCACTGTTGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCTCCTGGG  
GTGCTTGTGGCCTCCTACCCACTTCTGCTCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
CAGCGTTCTGCTGAACCTCCCTCCCTCAAGCTGCCCTGTCCCAGGAGACCGCAGTGTG  
CTACCTGTGTGCAAGCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCAGG  
GGCGCCACTCATTGTTATGATGGGTACATTCACTCTCAGGAGGTGGCTGTCCACCAAAAT  
GAGCATTCAAGGCTGCGTGGCCAACCTCCAGCTTGTGAACCACACCAGACAAATCG  
GGATCTTCTCTGCGCGTGAGAACGCGTATGTGCAAGCTCCTGCCTCTCAGCATGAGGGAGGT  
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCAGCGCTGTG  
GTGGGGAGTGGTTGCCCTCCTGCTTAACTCTATTACCCCCACGATTCTCACCGCTGCTGA  
CCACCCACACTCAACCTCCCTGACCTCATAACCTAATGGCCTGGACACCAGATTCTTC  
CCATTCTGTCCATGAATCATCTTCCCCACACACAATTCACTATCTACTCACCTAACAGCA  
ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCTATGGGAGAGGGACGCTGGAGGGAGTG  
GCTGCATGTATCTGATAATACAGACCCTGTCCTTCA

003218212201

## **FIGURE 10**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847  
><subunit 1 of 1, 437 aa, 1 stop  
><MW: 46363, pI: 6.22, NX(S/T): 3  
MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTCDSGLGCQDTLMLI  
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCPVCLSMEGCLEGTEEICPKGTTHCYDGLRLRGGGIFSNLRVQGCMPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTSNTEMCEVGQVCQETL  
LLIDVGLTSTLVGTLKGCTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSVLLN  
SLPPQAAVPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGAEGLSLTWGVGLALAPALWWGVVCPSC
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 243-260

**N-glycosylation sites.**

amino acids 46-49, 189-192, 382-385

**Glycosaminoglycan attachment sites.**

amino acids 51-54, 359-362

**N-myristoylation sites.**

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,  
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,  
360-365, 361-366, 388-393, 408-413, 419-424

## **FIGURE 11**

CGACG**ATG**CTACGCGGCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCCCTG  
GCTGCGGCCGCTGCTCTCGCTGCGCTGCTCTCTTAGAGCCGAGGGACCCGGTGGC  
CTCGTCGCTCAGCCCCATTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCGTGCTAT  
TGTGGGCCCCGAGGCTCCGTGGCGGGACCCCTGAGCTGCTGGAGGGACCTGCACCCGGTG  
CAGCTGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT  
GAGGCAGCTGCACGGGTTGCTGCAGGCCGGTCCAGGGATGGGGCTAGTAGTACCG  
GCAGCCGCGACCTGGGTGCAGCGCTGGCGACTGGCCTTGTGGTACCGGACTGGATGGAC  
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGCTGGCCTCGCT  
CTTCCC GGCCCTTTCAAGCGTGAGAACTACGCCGCCTGCGGCTCATCACCAGTTCCAAGC  
ACCGCTGCATGGATAGCAGGCCGCCTCCTGCAGGGCTGTGGCAGCACTACCACCCCTGGC  
TTGCCGCCGGACGTCGCAGATATGGAGTTGGACCTCCAACAGTTAATGATAAACTAAT  
GAGATTTTTGATCAGTGTGAGAAGTTTAACGAAGTAGAAAAAAATGCTACAGCTTTT  
ATCACGTGGAAGCCTCAAAACTGGACAGAAATGAGAACATTAAAAAGTTGCAGCT  
ACTTTGCAAGTGCCAGTAAATGATTAAATGAGATTAACTCAAGTAGCCTTTTACCTG  
TTCATTGACCTGGCAATTAAAGGTGTTAAATCTCCTGGTGTGATGTTTGACATAGATG  
ATGCAAAGGTATTAGAATATTAAATGATCTGAAACAATATTGAAAAGAGGATATGGGTAT  
ACTATTAAACAGTCGATCCAGCTGCACCTGTTAGGATATCTTCAGCACTGGACAAAGC  
AGTTGAACAGAAACAAAGGTCTCAGCCAATTCTCTCCAGTCATCCTCCAGTTGGTCATG  
CAGAGACTCTCTTCACTGCTTCTCATGGCTACTCTAAAGACAAGGAACCCCTAAC  
GCGTACAATTACAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGC  
CTGAACCTGATATTGTGCTTACCACTGTGAAATGCTAAGACTCCTAAAGAACATTCC  
GAGTCAGATGTTATTAAATGAAAAGGTGTTACCTTGGCTACTCACAAGAAACTGTTCA  
TTTATGAAGATCTGAAGAACCACTACAAGGACATCCTCAGAGTTGTCAAACCAAGTGAAGA  
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACT**TGA**TAACGTGAAACATT  
AATTCTTAGGAATCTGCAATGAGTGTGATTACATGCTTGTAAATAGGTAGGCAATT  
ACAGGAAGCTTTATATTACTTGAGTATTCTGTCTTTCACAGAAAACATTGGGTTCTC  
TCTGGGTTGGACATGAAATGTAAGAAAAGATTTCACTGGAGCAGCTCTTAAGGAGAA  
ACAAATCTATTAGAGAAACAGCTGGCCTGCAAATGTTACAGAAATGAAATTCTCCTAC  
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTCATAATAACACTTGAAAAGTGT  
GGAGTAACAAAATATCTCAGTTGGACCACCTTAACCTGATTGAACTGTCTAGGAAC  
AGATTGTTCTGCAGTTCTCTCTTCTCAGGTAGGACAGCTCTAGCATTCTTAATC  
AGGAATATTGTGGTAAGCTGGAGTATCACTCTGAAAGAAAGTAACATCTCAGATGAGAAT  
TTGAAACAAGAAACAGAGTGTGAAAAGGACACCTCACTGAAGCAAGTCGGAAAGTACAA  
TGAAAATAAATATTTGGTATTATTATGAAATATTGAACATTTCATAATTCTT  
TTTACTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATGTTGGACAATTAGCAAC  
AAGTCAGATAGTTAGAATCGAAGTTTCAAATCCATTGCTTAGCTAACTTTTCAATTCTGT  
CACTGGCTTCGATTTTATATTTCCTATTATGAAATGTATCTTGGTTGTTGATT  
TTCTTCTTCTTGTAAATAGTCTGAGTTCTGTCAAATGCCGTGAAAGTATTGCTATAA  
TAAAGAAAATTCTTGTGACTTTAAAAAAAAA

1003452-43323

## **FIGURE 12**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400
><subunit 1 of 1, 487 aa, 1 stop
><MW: 55051, pI: 8.14, NX(S/T): 2
MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLS
GPEAPWRDPELLEGTCVPQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGASSTGS
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMILLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL
```

**Important features:**

**Signal sequence**

amino acids 1-30

**N-glycosylation sites.**

amino acids 242-246, 481-485

**N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

**Endoplasmic reticulum targeting sequence.**

amino acids 484-489

## FIGURE 13

GGGACTACAAGCCGCCCGCTGCCGTGGCCCTCAGCAACCCTGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTCGCGCTGGCTGCCTGACTTCTCCGTGCTGCTGTTTCAGGGCTGCCTGATAAGGGCTGAAATC  
TCAAATCCAGCAATCGAACCCCCAGTGGTACAGGAATTGAAAGTGTGAACTGTCTGCATCATTACGATTGCG  
AGACAAGTGACCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAAACAAACACATATGTGTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTGTGAGGTCGAGAAATACTGGGAAGACATCCCTGAAGATCTGAAATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGTCGAGGTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCGGAAGGCTGTACCACTAGGCAAGATGGCAACACTGCG  
ACTGCCAGGAGACTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT  
CCAGAGCCAATCCCAGATTGCAATTCTCTTCCACTTAAACTCTGAAACAGGCACTTGGTGTTCAGTGTGCTG  
TTCACAAGGACGACTCTGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGAATTATGGGGGGTCTGGTGTCTGCTGTACTGCCCTGTA  
TCACGTTGGCATCTGCTGTGCATACAGCTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCACTCAGACACAAGTCATCGTTG  
TGATCTGAACCCCGGGTGTGGCTGAGAGCGCACAGAGCGACGTGACATACCTCTGCTAGAAACTCCTGCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTAGCAGCTTTGCTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTACTGAGTTGGGCTTAATCTGTTCTGGCCTGATTCCGCATGAGTATTAGG  
GTGATCTAAAGAGTTGCTCACGTAACGCCGTGCTGGCCCTGTAAGCCAGCATGTTACCACTGGTCGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCGAGCGCATCCGGCGGAACCCA  
GAAAAGGCTCTTACACAGCAGCCTTACTTCATGGCCCACAGACACCCACCGCAGTTCTTAAAGGCTCTG  
TGATCGGTGTTGCACTGTCATTGTGAGAAGCTTTGGATCAGCATTGTGAAACACCAAAATCAGGAAG  
GTAATTGGTTGCTGGAAGAGGGATCTGCTGAGGAACCTGCTTGTCCAACAGGGTGTAGGATTAAAGGAAA  
ACCTCGTCTTAGGCTAACGCTGAAATGGTACTGAAATATGCTTTCTATGGTCTTGTGTTATTTATAAAATT  
TACATCTAAATTGGCTAACGGATGTATTGATTATGAAAAGAAAATTCTATTAAACTGTAAATATATTG  
CATACAATGTTAACCTATTTTAAAGTTCAACTAACGGTAGAACGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAGAGTATTGCTAACAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTTCT  
CACACAAGTTTACGCTTTTACAAGGAAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCATCTCTCAAAAGAAACCTCTCAGGTTAGCTTGAAC  
GCCCTTCCTGAGATGACTAGGACAGTGTACCCAGAGGCCACCCAGAACGCCCTCAGATGTACACACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCCGTGTCTGCCAGGAGGCC  
GCCATCCTTGGGCCCTGGCAGTGGCTGTCCAGTGAGCTTACTCACGTGCCCTGCTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTCCATGTAGCGTCCAGCTTGGCTCTGTAACAGACCTCT  
TTTGGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTGTTAAAGTTGTTAATTATTGTT  
AAGATTGCTAACGGCAAAGGCAATTGCGAAATCAAGTGTCAAGTACAATAACATTAAAAGAAAATGGAT  
CCCACTGTTCTCTTGCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCAGGTGAAAGGCCCTGGCGGGAGGAAG  
TGAAACGCCCTGAATCAAAGCAGTTCTAACATTGACTTTAAATTTCTACCGCCGGAGACACTGCTCCATT  
TGTGGGGGGACATTAGCAACATCACTCAGAACGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC  
GCCGTGCTGGACTCAGGACTGAAAGTGTGTAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTC  
GAATGGCTCTCAACTCACCTGTCTTCAGCTTCCAGTGTCTGGTTTTACTTGACAGCTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTAGTTATGAAACACTTGCCGCAAGGCCCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGCCATCTGGATGCTTAGCATGCAAGTTC  
CCTCCATGGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTACGCTCCAGCCTC  
TCTTGGTTGTACAGTGTAGGGTAGCCTTATTGCCCCCTTCTTACACCTAAACCTTACACTAGTGCCA  
TGGGAAACCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACAGGGCTGTGATTCT  
GCCTTGGATGGATGGTGTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTTGTTAAC  
CTCATTATAAAAGCTCAAAAAACCCA

00031972-4202

## **FIGURE 14**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLCARLPDFLFFFRLGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

## **FIGURE 15**

CAGGACCAGGTCTCCTACGCTGGAGCAGCGGGGAGACAGCCACC**ATG**CACATCCTCGTGGCATGCCATGGTG  
ATCCTGCTGACGCTGGGCCCGCTCGAGCCGACAGCGAGTTCCAGGCCTGCTGGACATCTGGTTCCGGAG  
GAGAAGCCACTGCCAACCGCTTCCTGGTGGACACATCGGAGGAGGCCTGCTGTTCTGACTGGCTGAAGCTG  
CGCATGATCCGTTCTGAGGTGCTCCGCCTGGTGACGCCCTGAGGACCTGGAGGCCAGCAGCTGCTGCTG  
TTCGTGCAGTCGTTGGCATCCCCGTGTCAGCATGAGCAAACCTCCAGTCTGGACCAGGCAGTGGCCCAC  
GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCACCTGGTGGAGGTCCAGCATGAGC  
GGGCCCTCCGGAGGCCAGACTTCCACTCCTGCTCACAGCCTCCCTGCCGCCAGAGACAGCACAGAGGCA  
CCCAAACCAAAGAGCAGGCCAGAGCAGCCATAGGCCAGGGCCGATTCGGGTGGGGACCCAGCTCCGGGTGCTG  
GGCCCTGAGGAGCAGCCTGGCTGGCATGTTCCCTCAGATTTCCGCTCAGGCCGACCCCTGGTGGCAGAGCTCC  
AGTCCCCGCCCGTGGCCCTGCAGCAGGCCCTGGCCAGGAGCTGGCCCGTGTCCAGGGCAGGCC  
GAGGTGCCGGGCATCACGGTGCCTGCTGCAGGCCCTGCCACCCCTGCTCACGCTCCCCACACGGCGGTGCCCTG  
GTGATGTCATGACCGTAGCCACTTCCCTGGCCTGCCGCTGCTGCCAGCTGCTGCCAGTACCGCGCTGTGTG  
CCACAGGACACCGCTCTCCTCGCTTCTGAAGGTGCTCCTGCAGATGCTGAGTGGCTGGACAGCCCTGGC  
GTGGAGGGCGGGCCCTGCCGGCACAGCTCAGGATGCTGCCAGGCCAGGCCAGGCCAGGCTCAGGCC  
GTGCGAGGGGGCTCTGCCCTGGCCAGGCCCTGGCTCCGTAGGACCTGGAGGTGGTCAGCTCCACCGTC  
CGTGCCTGTCATGCCACCCCTGAGGTCTGGGAGCAGTGCAGCGTGGAGGCCAGCTGATCAGCAAAGTCTCCAG  
GGGCTGATCGAGGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTCTGCCACTGCCAGTGGCTG  
TCCCCGTTCCAGCCTGTAAGCCGTTGTTGGTGGAGCTCCCTGCTGCTGCCAGGAGGAGGCCCTGGCTGGG  
GGGAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGGCTGGGCCCTGTCAGGCCCTAGTGGACTGG  
CTGGAATGCTGGACCCCAGGTGGTCACTGAGCTGCCCCGACCTGACCCCTTCACTGCATCAGTCCAGTGG  
GGCAAAGGTCAAGGCCAGGTGCCCTCGTCCGCTCACCTCCTGACCCCTTCACTGCATCAGTCCAGTGG  
ACACTGCACCAGTCATCCAGTCTGCTGGCAAGAGCCGGAACAGAGGTTGACCCCTCTGCCCTCTGG  
TTCCCTGGCCTGCATCCATGTTCCCTGCATCTGGCAGGGCGGACCAGCGCACCCCGCAGAAGCGGG  
GAGCTGGTGCTGGGTCCAGGGCCGGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCGAGGCCAGCG  
AGCCAGGACGGGACACAGCCGCTGCAGCCTCATCCAGGCCGGTGTGCCCTGCTGCTCAGCTGCTGTGG  
GACGATGAGAGTGCAGGAAGGTGACGGAGCACCTGTCAGGCTGCATCCAGCAGTGGGAGACAGCGTGTGG  
AGGCCTGCCAGACCTCTCCTGCAGCTCTACAGCCGGAGCTGCGGGTGCCCTGAGGTCTTA  
CTGCACAGCGAAGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGACGACTCATCCACCGCTCATCAGCTC  
GCCGACACCAGCGACTCCGGCGTTGGAGAACCGAGGGCGGATGCCAGCATGCCCTGCCGAAGCTGG  
GCGCACCGCTGCTGCTCAGGCACCTGCCATGTCGGCGCTCTGCACGGCCGACCCACCTCAACTTC  
CAGGAGTTCCGGCAGCAGAACACCCTGAGCTGCTTCCCTGCACGTGCTGGCCTGAGCTGCTGCC  
GTGTTCCGCAGCGAGCACAGGGGGCGCTGTGGAGCTGCCTTCTGTCATCCGCTGCTGCTGAATTACAGG  
AAAGTCCCTCCGCATCTGGCTGCCATTCAACAAGTTGTCAGTTCATCCATAAGTACATTACCTACAATGCC  
CCAGCAGCCATCTCCTCTGCAGAACAGCAGCCACCCGCTCCACGACCTGTCCTCGACAACAGTGA  
CTGGTGAAATCCCTCTGCAGGGCTAGCCTGCCAGCAGGGAGCACAGGAGGCCCTGGACGAAGAG  
GGCGAGGAGGAGAGCTCAGCCGGCTCTGCCCTGGTCACTGCAGCTCCCTGTTCA  
ATGGCCCCCTACATGAAACGGTTCCGGGGCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGA  
CATAGACGAGATGTCGGCGAGACCCGAGATCCTGAGCTCTCTCGACCAACCTGCAGGGCTGATGAG  
CTGGCCGAGAACCTCGCCTTCAGCCTGCCCTGCGCTCCATGCAGAACAGCCCAGCATTGCAG  
CTGCCACGTTCATGTAAGCAGGCCAGGACTTGGAGGTGGTGCAGACGCCCTCCGGAACCTGC  
TACGCTCTCTGTGCCAAGAGCACGCCAGTGTGCTGCCACCGGCCCTCTGGCATGTACGCCAGATG  
GACCCAGCGCAGATCTCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATG**TGAG**CTGTGGCAGCCGA  
CCCCCTCCAAGCCCCGGCCGCTCCGGATCCTCGAGGCAAAGCCAGGAAGCGTGGCGTTGCTGG  
TCTGTCGAGGAGGTGAGGGCGCCAGGCCCTGAGGCCAGGCCAGGAGCAAACTCCAGGCC  
CTCGAGGCCCTGCCATGGGCTGGCATCAGGGGCCAGCAAGCCCTCATTCA  
CTCGAGGCCCTGGGACAGGCCCTGCCAGGCC  
AGCGGGGAGATCCCCCGGGCATGCCCTGGGCTGGTTGAATGAAACGACCTGA  
ACTGTCAA

2003-185-2-13694

## FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTGPRAADDSEFQALLDIWFPPEEKPLPTAFLVDTSEEALLLPDWLKLRM  
IRSEVLRLVDAALQDLEPQQQLLFFQSGFIPVSSMSKLLQFLDQAVAHDQPQTLEQNIMDKNY  
MAHLVEVQHERGASGGQTFHSLLTASLPPRDSTEAPPKSSPEQPIGQGRIRVTQLRVLG  
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL  
ATLLSSPHGGALVMSMHRSHFLACPLLRLQCQYQRCVPQDTGFSSLFLKVLQMLQWLDSRG  
VEGGPLRQLRMLASQASAGRRLSDVRGGLLRLAEALAFRQDLEVSVSTRAVIATLRSGEQ  
CSVEPDLSKVLQGLIEVRSPHLEELLTAFFSATADAASPFPACKPVVVVSSLLLQEEEPLA  
GGKPGADGGSLEAVRLGPSSGLLVDWLEMIDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR  
PYLLTLFTHQSSWPTLHQCIRVLLGKSREQRFDPSASLDFLWACIHVPRIWQGRDQRTPQKR  
REELVLRVQGPTELISLVELILAEAEATRSQDGDTAACSLIQARLPLLLSCCCGDDESVRKVTE  
HLSGCIQQWGDSDLGRRCRDLLLQQLYLRPELRVPEVLLHSEGAASSSVCKLDGLIHRFI  
TLLADTSRDSRALENRGADASMACRKLAVALHPLLLRLPMIAALLHGRTHLFNFQEFRQQNHL  
SCFLHVGLLELLQPHVFRSEHQGALWDCLLSFIRLLNYRKSSRHLAAFINKFVQFIHKYI  
TYNAPAAISFLQKHADPLHDLSFDNSDLVMLKSLLAGLSLPSRDDRDRGLDEEGEEESSAG  
SLPLVSVSLFTPPLTAAEMAPYMKRLSRGQTVEDLLEVLSIDEDEMRRRPEILSFFSTNLQRL  
MSSAECCRNLAFSLALRSMQNNSPSIAAFLPTFMYCLGSQDFEVVQTALRNLPEYALLCQE  
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

**Important features:**

**Signal peptide:**

amino acids 1-16

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

**N-myristoylation sites.**

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,  
665-671, 698-704

**Amidation sites.**

amino acids 329-333, 634-638

## FIGURE 17

CCGGGCCATGCAGCCTGGCCCCGGCGCCGCCGCGCACCGAGGAGATGAGGGCTCCGC  
AATGGCACCTTCCTGACGCTGCTCTTCTGCCTGTGCGCCTTCCTCGCTGTCTGGTA  
CGCGGCACTCAGCGGCCAGAAAGGCAGCTTGAGCAGTTACCAGCGGAGTTCTGGCGC  
TGCGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTAACCTG  
GTGCTGGACGAGATCAAGAGGGCCGTGTCAAGAAAGGCAGGCGCTGCGAGACGGAGACGGCAA  
TCGCACCTGGGGCCGCTAACAGAGGACCCCCGATTGAAGCCGTGGAACGGCTCACACCGGC  
ACGTGCTGCACCTGCCAACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT  
CTGCAGCCCGGGTGCCTGGGCCAGGGCCGACCGGAGTGTGCGGTGATGGGCATCCC  
GAGCGTGCGGCGCAGGGTGCACCTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC  
TGAGCCCGAGGAGAAGGAGGACTCGGTATCGTGGCTGATGCCGAGACTGACTCACAG  
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGGTCCCCACGGAGATCCATTCTGGGCT  
CCTGGAGGTCATCTCACCCCTCCCCCCTAACCTGACTTCTCCCGCTCCGAGAGTCCT  
TTGGGGACCCAAGGAGAGACTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCCTC  
ATGATGTACGCGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA  
GCCCAACTACCTGAGCACCATGAAGAACTTGCACTGCAGCAGCCTTCAGAGGACTGGATGA  
TCCTGGAGTTCTCCCAGCTGGCCTCATGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG  
ATTGTAGAGTTCATCTCATGTTCTACCGGACAAGCCATCGACTGGCTCTGGACCATA  
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA  
ACCTGCGGATCCGCTCAAACCGTCCCTTCCAGCACGTGGGACTCACTCCTCGTGGCT  
GGCAAGATCCAGAAACTGAAGGACAAAGACTTGGAAAGCAGGGCGCTGCGGAAGGAGCATGT  
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATAACGACTTCACCCCTGGAGAAAG  
CCTACCTGCGCGAGGACTTCTCTGGGCTTCACCCCTGCCGCCGGGACTTCATCCGCTTC  
CGCTTCTCCAACCTCTAACAGACTGGAGCGGTTCTTCCCGCAGTGGGAACATCGAGCACCC  
GGAGGACAAGCTCTCAACACAGCTGTGGAGGTGCTGCCCTCGACAACCCCTCAGTCAGACA  
AGGAGGCCCTGCAGGAGGGCCGACCGCACCCCTCCGGTACCCCTGGAGCCCGACGGCTAC  
CTCCAGATCGGCTCCTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTCGGCC  
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCTGTGTGGGTATTCTGAGCGAGA  
TCTTCCTGAAAAAGGCCGACTAAGCTGGGGCTCTGAGGGTACCCCTGTGGCCAGCCTGAA  
GCCCAACATTCTGGGGGTGTCGTCAGTGCCTCCCCGGAGGGCCAGATAACGGCCCCGCCAA  
AGGGTTCTGCCTGGCGTGGGCTTGGGCCCTGGGTCCGCCGCTGGCCGGAGGCCCTA  
GGAGCTGGTGCCTGCCCGCCCGCCGGCGAGGAGGCAGGGCCGGAGGCCCTACACTGTGCC  
TGAGGCCCGGAACCGTTCGCACCCGGCTGCCCAAGTCAGGCCGTTAGAAGAGCTTTAC  
TTGGGCGCCGCCGTCTGGCGCGAACACTGGAATGCATATACTACTTTATGTGCTGTGTT  
TTTATTCTGGATACATTGATTTTACGTAAGTCCACATATACTTCTATAAGAGCGTG  
ACTTGTAAATAAGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

## **FIGURE 18**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307
><subunit 1 of 1, 548 aa, 1 stop
><MW: 63198, pI: 8.10, NX(S/T): 4
MRLRNGTFLTLLLFCFLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRLHAAEQESLKRSK
ELNLVLDEIKRAVSERQALRGDGDNRTWGRLEDPRLKPNNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRTGVSVVMGIPSVRREVHSYLTDLHSLISELSPQEKEDESVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVRWRTKQNLD
YCFLMMYAQSkgIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGTH
SSLAGKIQKLKDGFQALRKEHVNPPEVSTSLKTYQHFTLEKAYLREDFFWAFTPAAGD
FIRFRFFQPLRLERFFFSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAGPLEALRLSIQTDSPVWVILSEIFLKKAD
```

**Important features:**

**Signal sequence**

amino acids 1-23

**N-glycosylation sites.**

amino acids 5-9, 87-91, 103-107, 465-469

**N-myristoylation sites.**

amino acids 6-12, 136-142, 370-376, 509-515